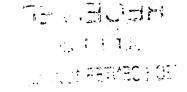


Fig. 2



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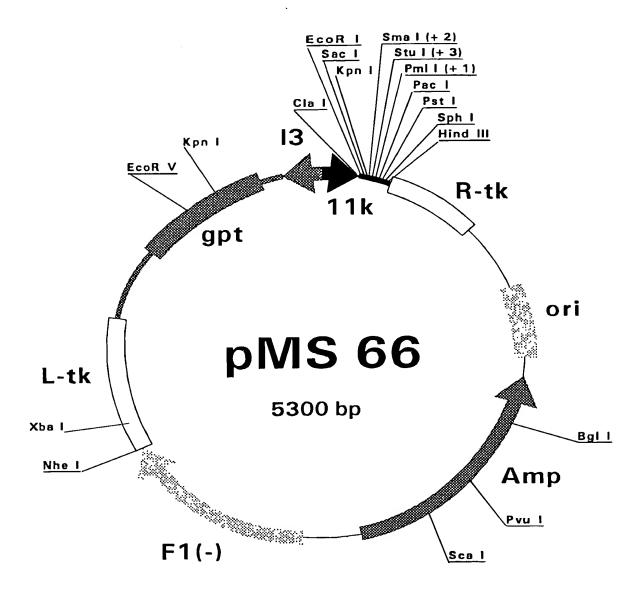


Fig. 3

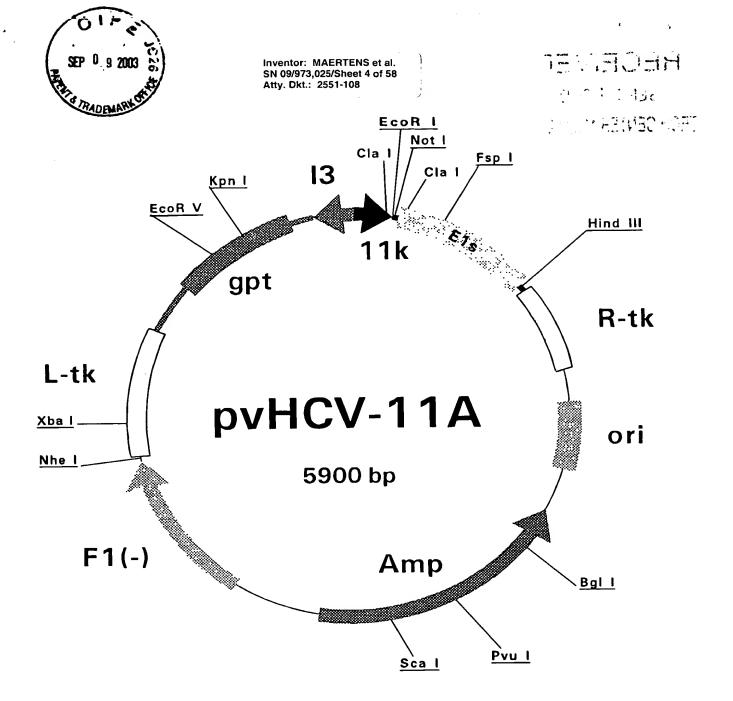


Fig. 4

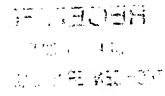
Anti-E1 levels in NON-responders to IFN treatment

Series 1

N/S

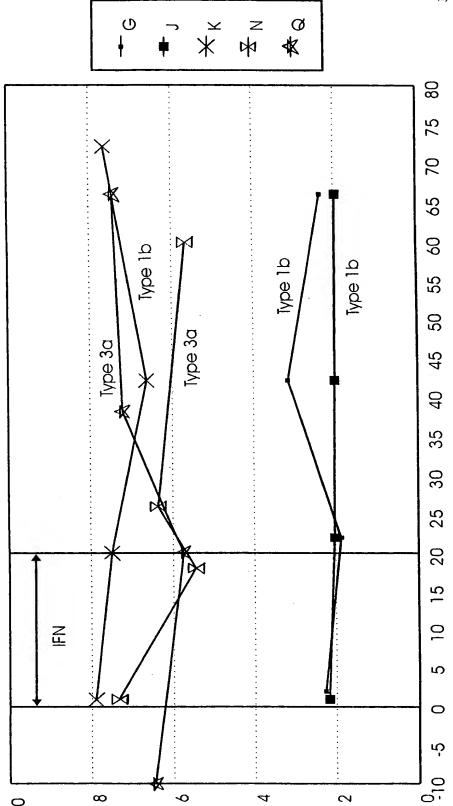
9

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weeks after start of treatment

Fig. 5



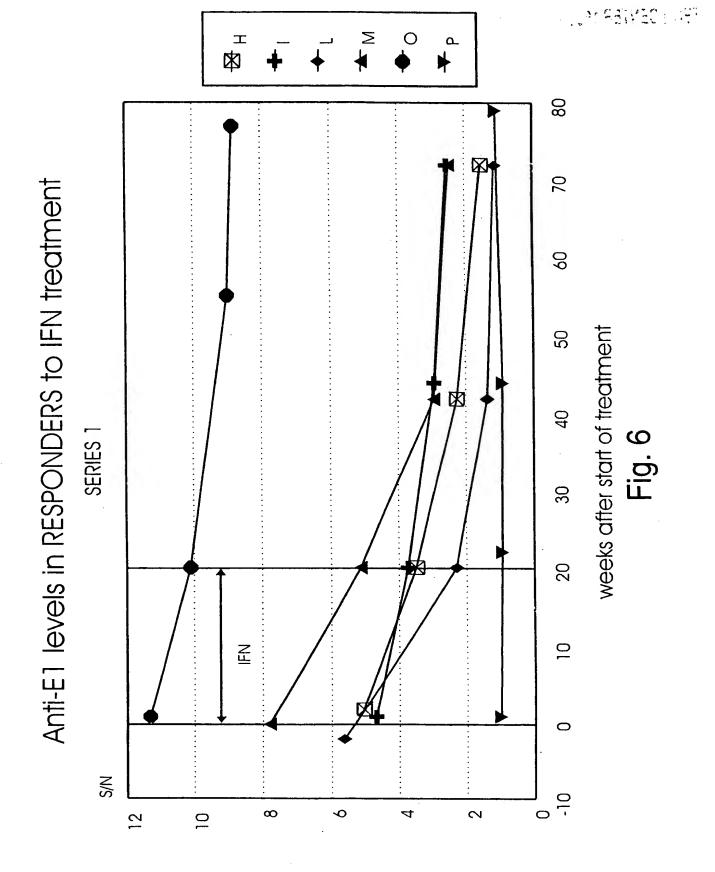
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Anti-E1 levels in patients with COMPLETE response to IFN

SERIES 2

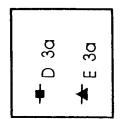
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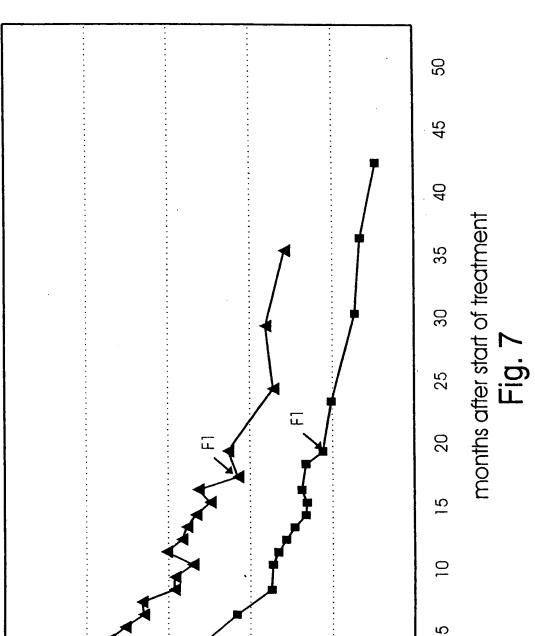
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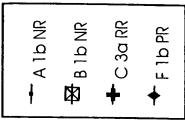


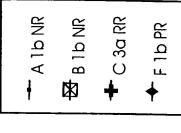
Anti-E1 levels in INCOMPLETE responders to IFN treatment

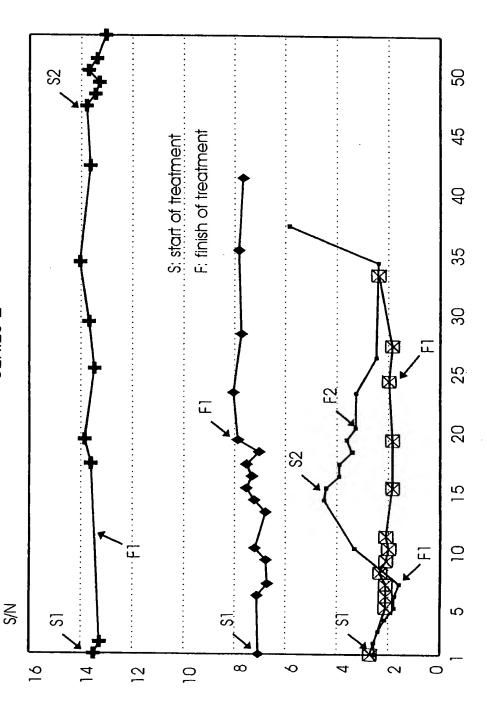
SERIES 2

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months after start of treatment Fig. 8

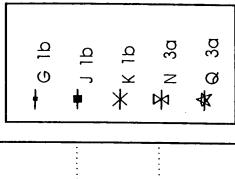
10-12-51 KID-13-7

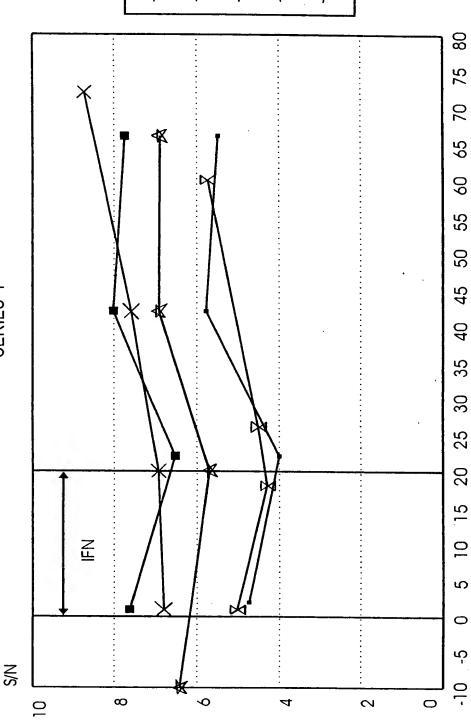


Anti-E2 levels in NON-RESPONDERS to IFN treatment

SERIES 1

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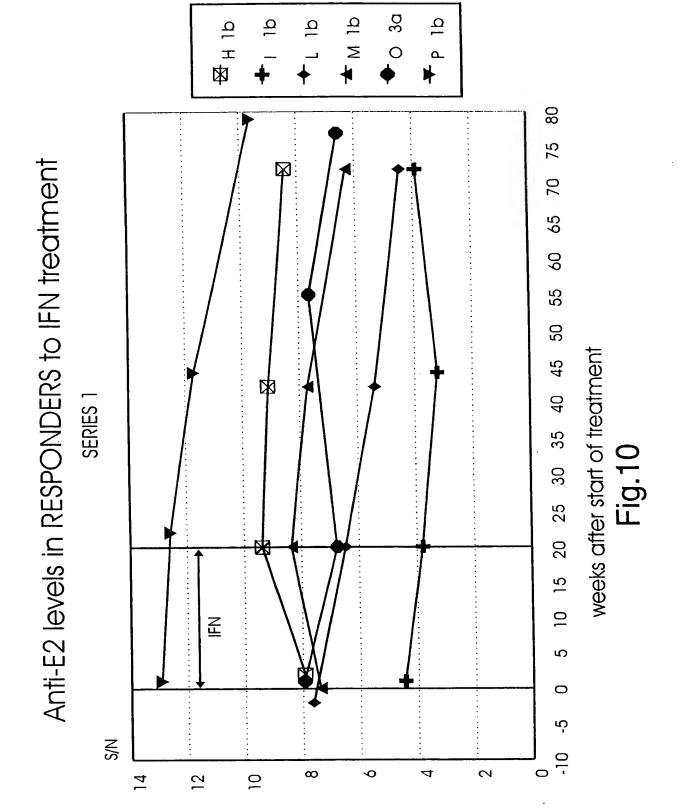


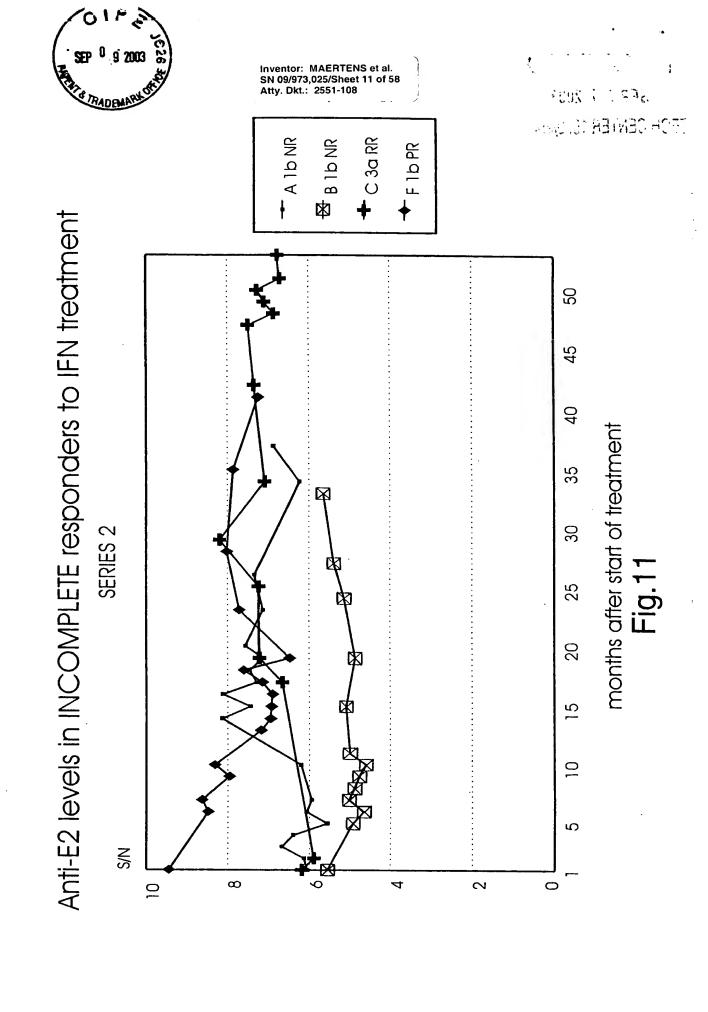
weeks after start of treatment Fig. 9



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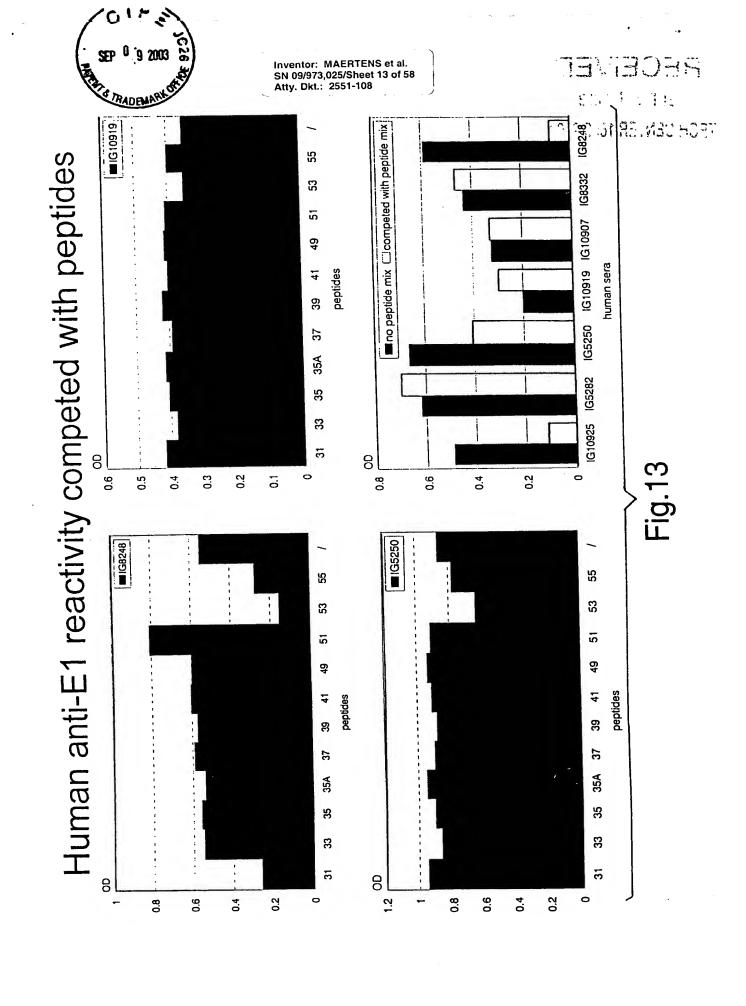
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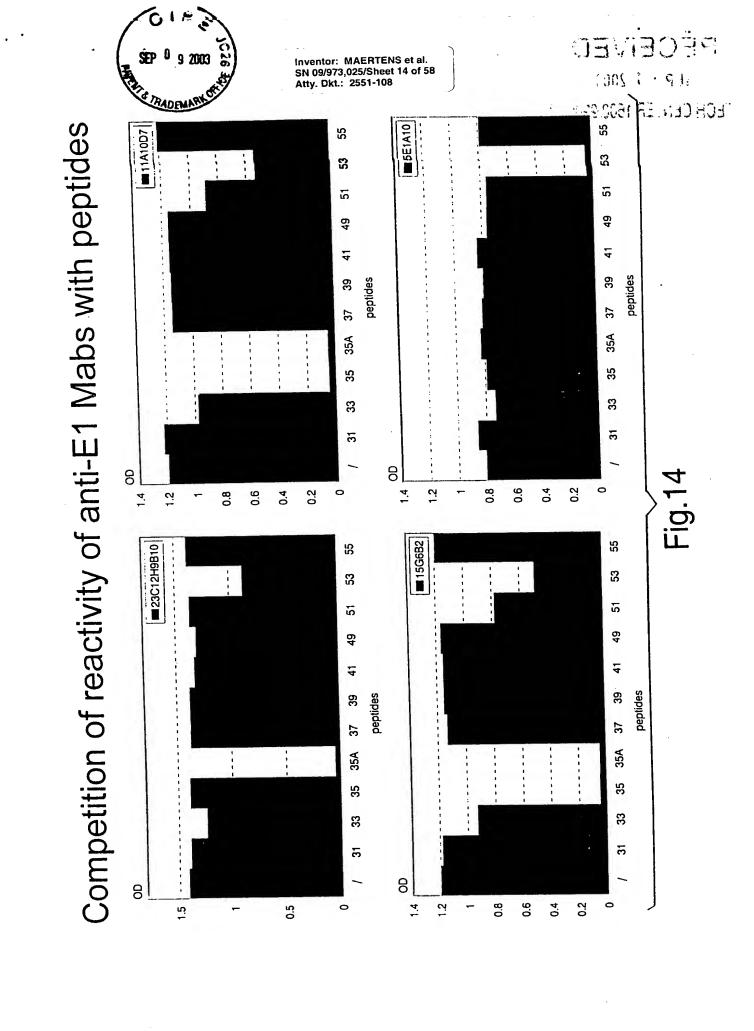
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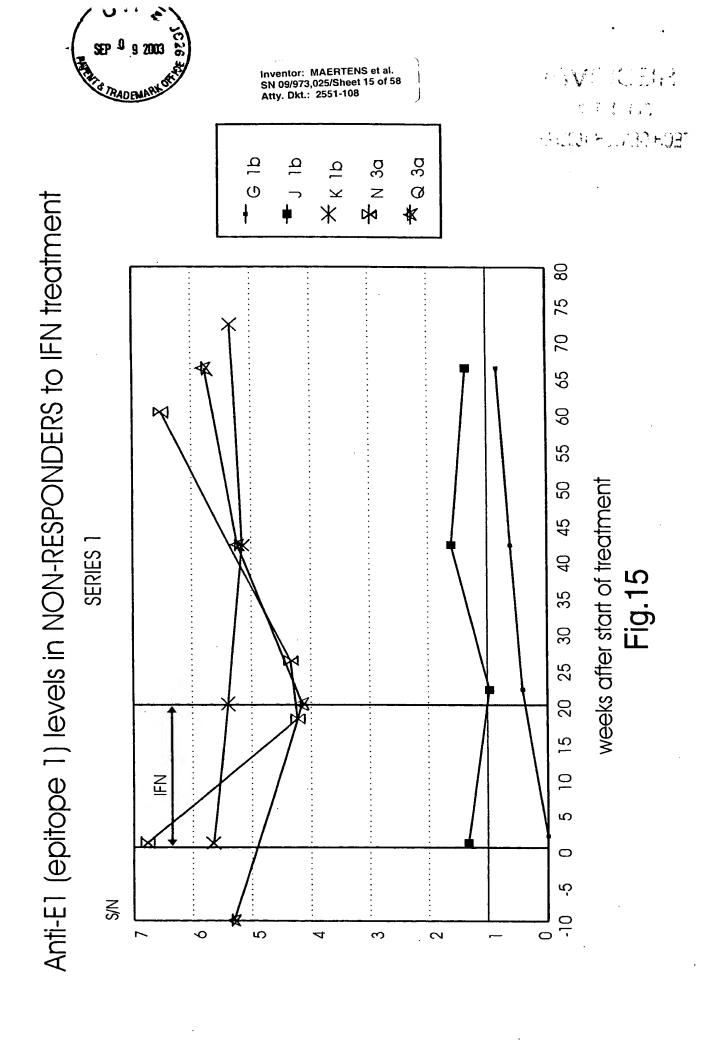
Anti-E2 levels in COMPLETE responders to IFN treatment

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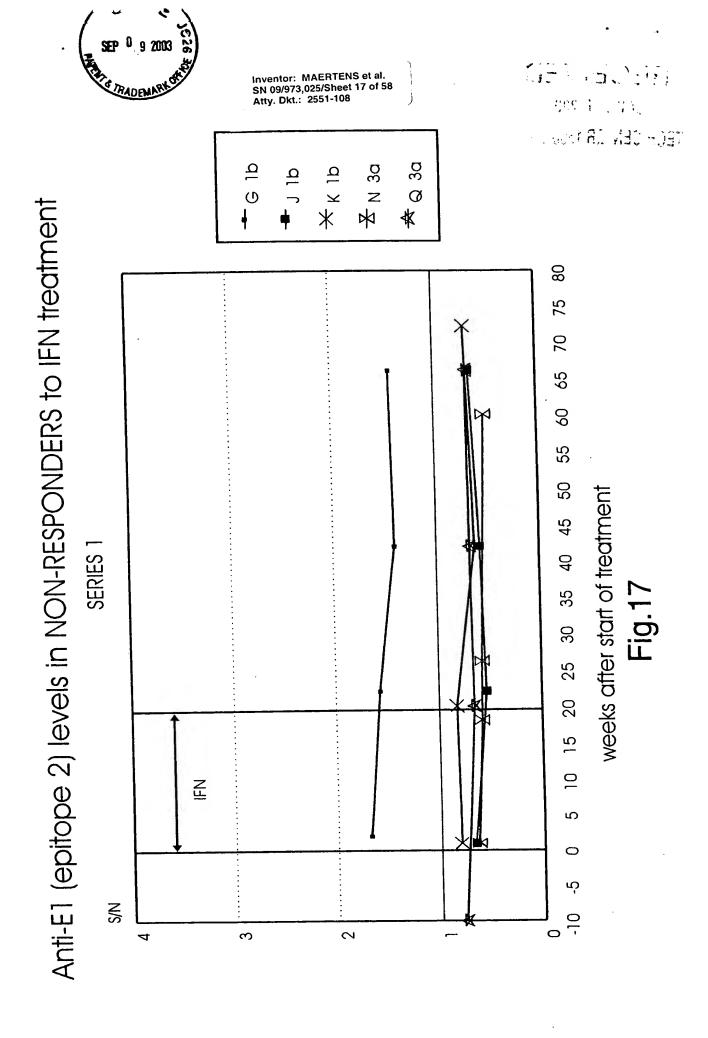
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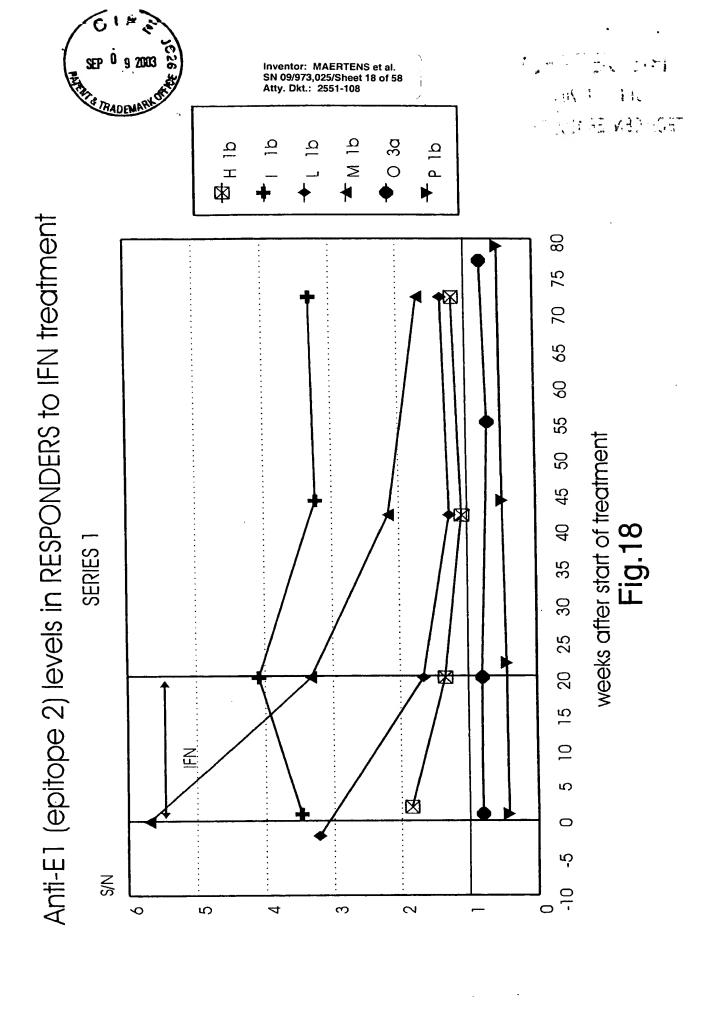


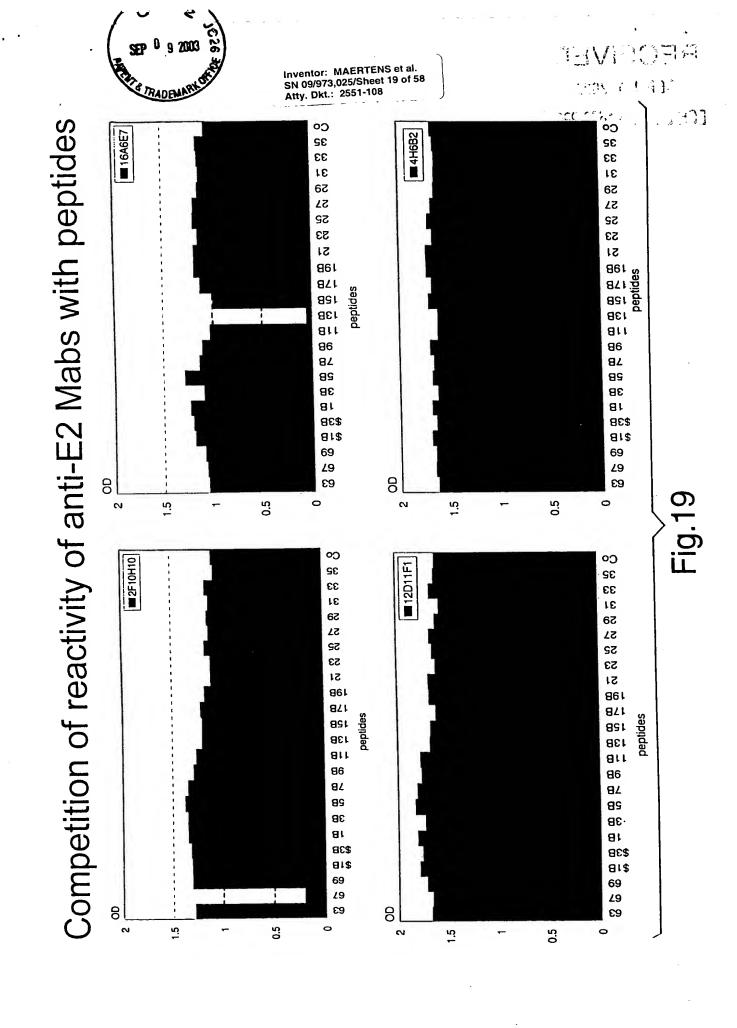


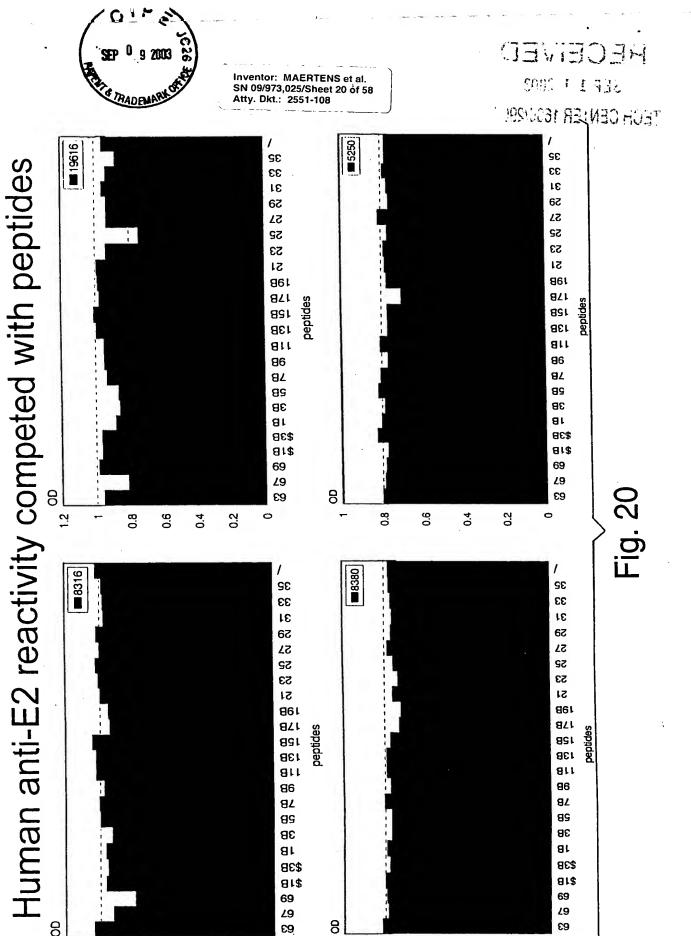


Inventor: MAERTENS et al. SN 09/973,025/Sheet 16 of 58 Atty. Dkt.: 2551-108 THE IENCES FOR 本 di H ₩ N 1b ►O 3a Anti-E1 (epitope 1) levels in RESPONDERS to IFN treatment 80 10 15 20 25 30 35 40 45 50 55 60 65 70 75 weeks after start of treatment Fig.16 SERIES 1 王 S ၯ S/N ω 2 Q ~ 4 0









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9.0

0.4

0.2

9.4

0.2



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## Fig. 21A

5' GGCATGCAAGCTTAATTAATT3' (SEQ ID NO 1)
3'ACGTCCGTACGTTCGAATTAATTAATCGA5' (SEQ ID NO 94)

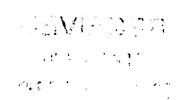
### SEQ ID NO 3 (HCCI9A)

#### SEQ ID NO 5 (HCCI10A)



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Fig. 21B



#### SEQ ID NO 7 (HCCI11A)

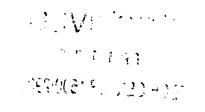
#### SEQ ID NO 9 (HCCI12A)

### SEQ ID NO 11 (HCCI13A)



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Fig. 21C



GCCCTGCGTTCGGGAGGGCAACTCCTCCCGTTGCTGGGTGGCGCTCACTCCCACGCTC
GCGGCCAGGAACGCCAGCGTCCCCACAACGACAATACGACGCCACGTCGATTTGCTC
GTTGGGGCTGCTTTCTGTTCCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTT
CCTTGTTTCCCAGCTGTTCACCTTCTCACCTCGCCGGCATCAAACAGTACAGGACTGCA
ACTGCTCAATCTATCCCGGCCATGTATCAGGTCACCGCATGGCTTGGGATATGATGAT
GAACTGGTAATAG

#### SEQ ID NO 13 (HCCI17A)

SEQ ID NO 15 (HCPr51)
ATGCCCGGTTGCTCTTTCTCTATCTT

SEQ ID NO 16 (HCPr52)
ATGTTGGGTAAGGTCATCGATACCCT

SEQ ID NO 17 (HCPr53)
CTATTAGGACCAGTTCATCATATCCCA

SEQ ID NO 18 (HCPr54)
CTATTACCAGTTCATCATCATATCCCA

SEQ ID NO 19 (HCPr107)
ATACGACGCCACGTCGATTCCCAGCTGTTCACCATC



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Fig. 21D



SEQ ID NO 20 (HCPr108)
GATGGTGAACAGCTGGGAATCGACGTGGCGTCGTAT

### SEQ ID NO 21 (HCCI37)

#### SEQ ID NO 23 (HCCl38)

#### **SEQ ID NO 25 (HCCI39)**

ATGTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA
TTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCCTGGCGCATGGCGTCCG
GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT



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## Fig. 21E

ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG
CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT
GAGGCAGCGGACATGATCATGCACACCCCCGGGTGCCTGCGTTCGGGAGAAC
AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG
TCCCCACCACGACAATACGACGCCACGTCGATTCCCAGCTGTTCACCATCTCGCCTCG
CCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGGCCACATAACGGGT
CACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACGGCCCTGGTGGTAT
CGCAGCTGCTCCGGATCCTCTAATAG

### SEQ ID NO 27 (HCCI40)

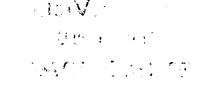
#### SEQ ID NO 29 (HCCl62)

ATGGTAAGGTCATCGATACCCTTACGTGCGGATTCGCCGATCTCATGGGGTACATCC
CGCTCGTCGGCGCTCCCGTAGGAGGCGTCGCAAGAGCCCTTGCGCATGGCGTGAGGGC
CCTTGAAGACGGGATAAATTTCGCAACAGGGAATTTGCCCGGTTGCTCCTTTTCTATTT
TCCTTCTCGCTCTGTTCTCTTGCTTAATTCATCCAGCAGCTAGTCTAGAGTGGCGGAAT
ACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTATTGTGTACGAGGC
CGATGACGTTATTCTGCACACACCCGGCTGCATACCTTGTGTCCAGGACGCAATACA
TCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAAGTACGTCGGAGCAACCA
CCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGCCACGATGTGCTCTGC
GCTCTACGTGGGTGACATGTGTGGGGCTGTCTTCCTCGTGGGACAAGCCTTCACGTTCA
GACCTCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCT
TTCAGGACATCGAATGGCTTGGGATATGATGATGATGAACTGGTAATAG



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Fig. 21F



SEQ ID NO 31 (HCCl63)

ATGGGTAAGGTCATCGATACCCTAACGTGCGGATTCGCCGATCTCATGGGGTATATCC
CGCTCGTAGGCGCCCCATTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGT
CCTTGAGGACGGGGTAAACTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCT
TTATTCTTGCTCTTCTCTCGTGTCTGACCGTTCCGGCCTCTGCAGTTCCCTACCGAAATG
CCTCTGGGATTTATCATGTTACCAATGATTGCCCAAACTCTTCCATAGTCTATGAGGCA
GATAACCTGATCCTACACGCACCTGGTTGCGTGCCTTGTGTCATGACAGGTAATGTGA
GTAGATGCTGGGTCCAAATTACCCCTACACTGTCAGCCCCGAGCCTCGGAGCAGTCAC
GGCTCCTCTTCGGAGAGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCTCCGCG
TTATACGTAGGAGACCGCTGTGGGGCCACTATTCTTGGTAGGCCAAATGTTCACCTATA
GGCCTCGCCAGCACGCTACGGTGCAGAACTGCAACTGTTCCATTTACAGTGGCCATGT
TACCGGCCACCGGATGGCATGGGATATGATGATGAACTGGTAATAG

SEQ ID NO 33 (HCPr109)
TGGGATATGATGATGAACTGGTC

SEQ ID NO 34 (HCPr72)
CTATTATGGTGGTAAKGCCARCARGAGCAGGAG

#### SEQ ID NO 35 (HCCL22A)



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## Fig. 21G

CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT
TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG
AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG
TCTACAACAGAGTGGCAGATACTGCCCTGTTCCTTCACCACCCTGCCGGCCCTATCCA
CCGGCCTGATCCACCTCCATCAGAACATCGTGGACGTGCAATACCTGTACGGTGTAGG
GTCGGCGGTTGTCTCCCTTGTCATCAAATGGGAGTATGTCCTGTTGCTCTTCCTT
GGCAGACGCGCGCATCTGCGCCTGCTTATGGATGATGCTGCTGATAGCTCAAGCTGAG
GCCGCCTTAGAGAACCTGGTGGTCCTCAATGCGGCGGCCGTGGCCGGGGCGCATGGC
ACTCTTTCCTTCCTTGTGTTCTTCTGTGCTGCCTGGTACATCAAGGGCAGGCTGGTCCC
TGGTGCGGCATACGCCTTCTATGGCGTGGCCGCTGCTCCTTCTCTTCTTCC
CACCACGAGCTTATGCCTAGTAA

#### SEQ ID NO 37 (HCCI41)

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGGG CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT TTGCCGGCGTCGACGGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CGACTCGGATGTGCTGATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGGCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA TCGGGGGGCCGCCACCTGACCTGCCCCACTGACTGTTTTCGGAAGCACCC CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG 

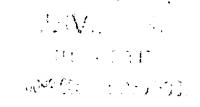
### **SEQ ID NO 39 (HCCI42)**

GATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCATTGGGGAGTCCTGGCGGG CCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCT



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Fig. 21H



TTGCCGGCGTCGACGGGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCA GGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACAC AGGGTTCTTTGCCGCACTATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAG CGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTT ACACTGAGCCTAACAGCTCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACC GTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCC CTGTTGTGGTGGGGACGACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAA CGACTCGGATGTGCTGATTCTCAACACACGCGGCCGCCGCGAGGCAACTGGTTCGGC TGTACATGGATGAATGCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACA CGAGGCCACCTACGCCAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTT CATTACCCATATAGGCTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGT TAGGATGTACGTGGGGGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCG AGGAGAGCGTTGTGACTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTG TCTACAACAGGTGATCGAGGGCAGACACCATCACCACCATCACTAATAG

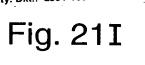
#### SEQ ID NO 41 (HCCl43)

ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG ATTCTCAACAACACGCGGCCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGG CAGAGCTTAATTAATTAG



**SEQ ID NO 43 (HCCI44)** 

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ATGGTGGGGAACTGGGCTAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACG GGCATACCCGCGTGTCAGGAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCT CTTTAGCCCCGGGTCGGCTCAGAAATCCAGCTCGTAAACACCAACGGCAGTTGGCAC ATCAACAGGACTGCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCAC TATTCTACAAACACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCG CTCCATCGACAAGTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGC TCGGACCAGAGGCCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCG CGTCTCAGGTGTGCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGAC GACCGATCGGTTTGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTG ATTCTCAACACCGCGGGCCGCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATG GCACTGGGTTCACCAAGACGTGTGGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCA ACAACACCTTGACCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGC CAGATGCGGTTCTGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGG CTCTGGCACTACCCCTGCACTGTCAACTTCACCATCTTCAAGGTTAGGATGTACGTGGG GGGCGTGGAGCACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGA CTTGGAGGACAGGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGGTGAT

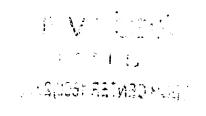
#### SEQ ID NO 45 (HCCL64)

CGAGGGCAGACACCATCACCACCATCACTAATAG



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Fig. 21J



#### SEQ ID NO 47 (HCCl65)

AATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGGGGTACA TTCCGCTCGTCGGCGCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCG GGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCT ATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAAGTGCG CAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTGTGTAT GAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGCCCTGCGTTCGGGAGAAC AACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCCAGCG TCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCCGGCTGCTTTCTG TTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTGTTCA CCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATCCCGG CCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTACAACG GCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGG GGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGC TAAGGTTTTGGTTGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGTGTCAG GAGGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGGTCGGC TCAGAAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACTGCCCT GAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAACACAA TTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGCTCCATCGACAAGTTCG CTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGGCCCTA CTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGTGCGGT CCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGGACGACCGATCGGTTTGGTGT CCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACACACGCGG CCGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCACCAAGA CGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGACCTGCC



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# Fig. 21K

#### SEQ ID NO 49 (HCCl66)

ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCA CAGGACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGC GCAGGGCCCCAGGTTGGGTGTCGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAAC CTCGTGGGAGGCGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGTAGGGCCTGGG CTCAGCCCGGGTACCCTTGGCCCCTCTATGGCAATGAGGGCATGGGGTGGGCAGGATG GCTCCTGTCACCCCGCGCCTCTCGGCCTAGTTGGGGCCCTACAGACCCCCGGCGTAGG TCGCGTAATTTGGGTAAGGTCATCGATACCCTTACATGCGGCTTCGCCGACCTCGTGG GGTACATTCCGCTCGTCGGCGCCCCCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGG CGTCCGGGTTCTGGAGGACGGCGTGAACTATGCAACAGGGAATTTGCCCGGTTGCTCT TTCTCTATCTTCCTCTTGGCTTTGCTGTCCTGTCTGACCGTTCCAGCTTCCGCTTATGAA GTGCGCAACGTGTCCGGGATGTACCATGTCACGAACGACTGCTCCAACTCAAGCATTG GAACAACTCTTCCCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCAGCTAGGAACGCC AGCGTCCCCACCACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTT TCTGTTCCGCTATGTACGTGGGGGACCTCTGCGGATCTGTCTTCCTCGTCTCCCAGCTG TTCACCATCTCGCCTCGCCGGCATGAGACGGTGCAGGACTGCAATTGCTCAATCTATC CCGGCCACATAACGGGTCACCGTATGGCTTGGGATATGATGATGAACTGGTCGCCTAC AACGGCCCTGGTGGTATCGCAGCTGCTCCGGATCCCACAAGCTGTCGTGGACATGGTG GCGGGGCCCATTGGGGAGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACT GGGCTAAGGTTTTGGTGATGCTACTCTTTGCCGGCGTCGACGGGCATACCCGCGT GTCAGGAGGGCAGCAGCCTCCGATACCAGGGGCCTTGTGTCCCTCTTTAGCCCCGGG



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# Fig. 21L

TCGGCTCAGAAATCCAGCTCGTAAACACCAACGGCAGTTGGCACATCAACAGGACT GCCCTGAACTGCAACGACTCCCTCCAAACAGGGTTCTTTGCCGCACTATTCTACAAAC ACAAATTCAACTCGTCTGGATGCCCAGAGCGCTTGGCCAGCTGTCGACAA GTTCGCTCAGGGGTGGGGTCCCCTCACTTACACTGAGCCTAACAGCTCGGACCAGAGG CCCTACTGCTGGCACTACGCGCCTCGACCGTGTGGTATTGTACCCGCGTCTCAGGTGT GCGGTCCAGTGTATTGCTTCACCCCGAGCCCTGTTGTGGTGGGGACGACCGATCGGTT TGGTGTCCCCACGTATAACTGGGGGGCGAACGACTCGGATGTGCTGATTCTCAACAAC ACGCGGCCGCGAGGCAACTGGTTCGGCTGTACATGGATGAATGGCACTGGGTTCA CCAAGACGTGTGGGGGCCCCCCGTGCAACATCGGGGGGGCCGGCAACACACCTTGA CCTGCCCCACTGACTGTTTTCGGAAGCACCCCGAGGCCACCTACGCCAGATGCGGTTC TGGGCCCTGGCTGACACCTAGGTGTATGGTTCATTACCCATATAGGCTCTGGCACTAC ACAGGTTCGAAGCCGCATGCAATTGGACTCGAGGAGAGCGTTGTGACTTGGAGGACA GGGATAGATCAGAGCTTAGCCCGCTGCTGCTGTCTACAACAGAGTGGCAGATACTGCC CTGTTCCTTCACCACCTGCCGGCCCTATCCACCGGCCTGATCCACCTCCATCAGAAC ATCGTGGACGTGCAATACCTGTACGGTGTAGGGTCGGCGGTTGTCTCCCTTGTCATCA AATGGGAGTATGTCCTGTTGCTCTTCCTTCTCCTGGCAGACGCGCGCATCTGCGCCTGC TTATGGATGATGCTGATAGCTCAAGCTGAGGCCGCCTTAGAGAACCTGGTGGTCC TCAATGCGGCGGCCGTGGCCGGGGCGCATGGCACTCTTTCCTTCTTGTGTTCTTCTGT GCTGCCTGGTACATCAAGGGCAGGCTGGTCCCTGGTGCGGCATACGCCTTCTATGGCG TGTGGCCGCTGCTCCTGCTTGCTGGCCTTACCACCACGAGCTTATGCCTAGTAA



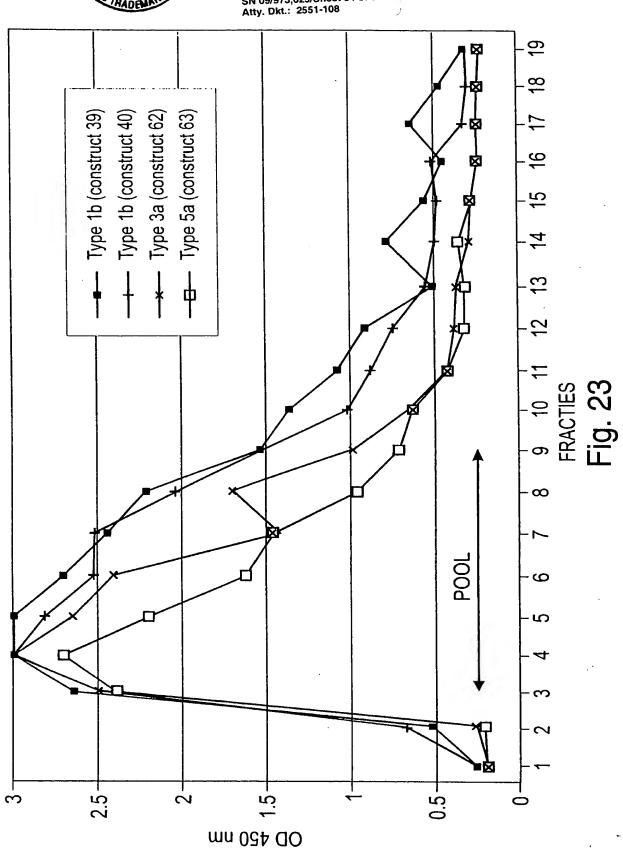
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Fig. 22

# OD measured at 450 nm construct

Fraction	volume dilution	39	40	62	63
		Туре	Type	Type	Type
		16	16	3a	5a
START	23 ml 1/20	2.517	1.954	1.426	1.142
FLOW THR		0.087	0.085	0.176	0.120
1	0.4 ml 1/200	0.102	0.051	0.048	0.050
2		0.396	0.550	0.090	0.067
3		2.627	2.603	2.481	2.372
4		3	2.967	3	2.694
5		3	2.810	2.640	2.154
6		2.694	2,499	1.359	1.561
7		2.408	2.481	0.347	1.390
8		2.176	1.970	1.624	0.865
ò		1.461	1.422	0.887	0.604
10		1.286	0.926	0.543	0.519
11		0.981	0.781	0.294	0.294
12		0.812	0.650	0.249	0.199
13		0.373	0.432	0.239	0.209
14		0.653	0.371	0.145	0.184
15	•	0.441	0.348	0.151	0.151
16		0.321	0.374	0.098	0.106
17		0.525	0.186	0.099	0.108
18		0.351	0.171	0.083	0.090
19		0.192	0.164	0.084	0.087
• /		0.172	2.101	0.501	0.007

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Fig. 24

# OD measured at 450 nm

construct								
volume	dilution	39 Type 1b	40 Type 1b	62 Type 3a	63 Type 5a			
250 <i>μ</i> Ι	1/200	0.072 0 109 0 279 0.093 0 080 0.251 3 3 3 2 227 0 263 0.071 0.103 0 045 0.045 0.045 0 046 0.045	0 130 0 293 0 249 0.151 0.266 0 100 1 649 3 3 3 1.921 0.415 0.172 0.054 0.045 0.045 0.047 0.045 0.047	0.096 0.096 0.084 0.172 0.297 0.438 0.457 0.722 2.528 3 2.849 1.424 0.356 0.154 0.096 0.044 0.045 0.045 0.045 0.046 0.047 0.050	0.051 0.052 0.052 0.054 0.056 0.048 0.066 0.889 2.345 2.580 1.333 0.162 0.064 0.057 0.051 0.046 0.040 0.048 0.057 0.057			
		0.046	0.049	0.048	0 049			
			volume dilution 39 Type 1b  250 μl 1/200 0.072 0 109 0 279 0.093 0 080 0.251 3 3 3 3 2 227 0 263 0.071 0.103 0 045 0.043 0.045 0.045 0.045 0.045 0.045	volume dilution 39 40 Type Type 1b 1b  250 μl 1/200 0.072 0 130 0 109 0 293 0 279 0 249 0.093 0.151 0 080 0.266 0.251 0 100 3 1 649 3 3 3 3 3 3 2 227 1.921 0 263 0.415 0.071 0.172 0.103 0.054 0 045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.048 0.045 0.048 0.045 0.048	volume       dilution       39 Type Type Type Type       Type Type Type         1b       1b       3a         250 μl       1/200       0.072 0 130 0.096         0 109 0 293 0 084 0 279 0 249 0 172 0.093 0.151 0 297 0.093 0.151 0 297 0.080 0.266 0.438 0.251 0 100 0 457 3 1 649 0.722 3 3 3 2.528 3 3 3 2.528 3 3 3 2.528 3 3 3 2.528 3 3 3 2.528 3 3 3 2.528 3 3 3 2.528 0.415 0.356 0.071 0.172 0.154 0.263 0.415 0.356 0.071 0.172 0.154 0.103 0.054 0.096 0.045 0			



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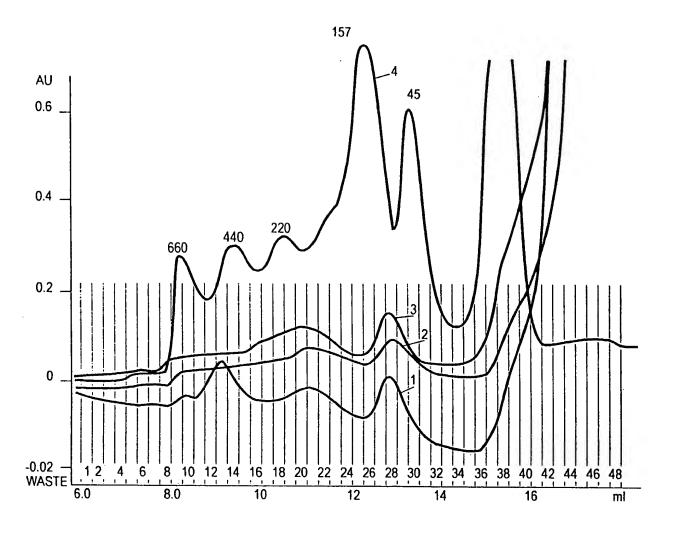


Fig. 25



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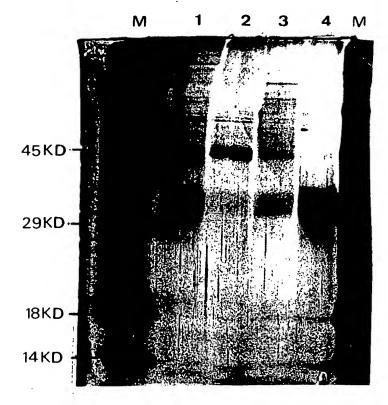


Fig. 26

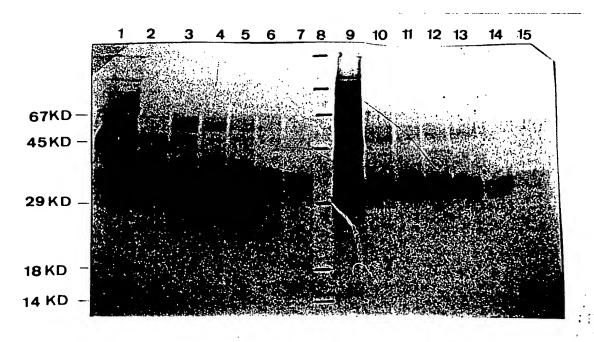
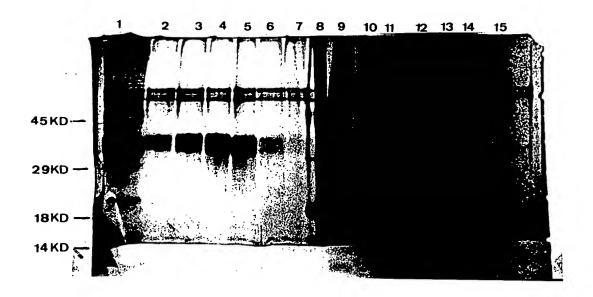


Fig.27



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# Fig.28

Fig.29 M

67 kD -

45 kD -

29 kD -

18 kD -

14 kD -

Lane 1: Crude Lysate

Lane 2: Flow through Lentil Chromatography

Lane 3: Wash with EMPIGEN Lentil Chromatography

Lane 4: Eluate Lentil Chromatography

Lane 5: Flow through during concentration lentil eluate

Lane 6: Pool of Elafter Size Exclusion Chromatography



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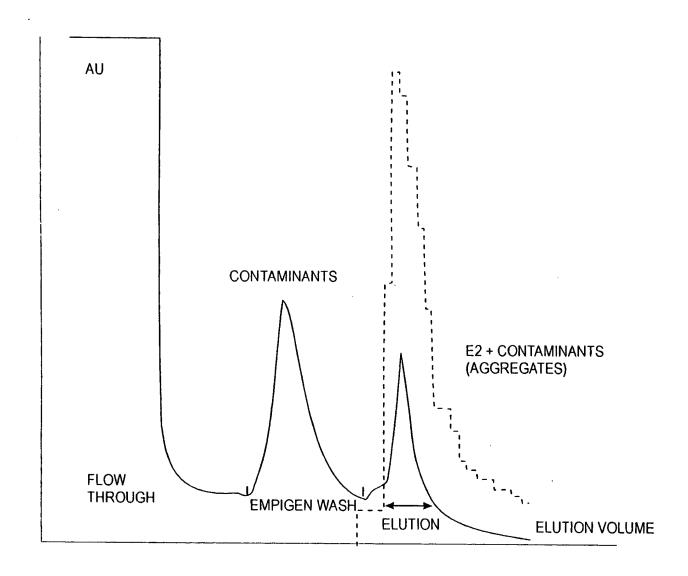


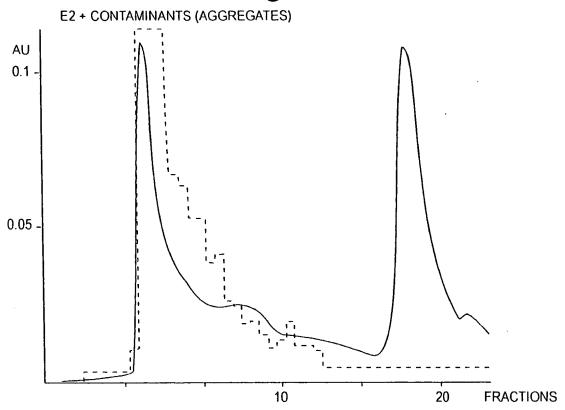
Fig. 30



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### **NON - REDUCED**

Fig. 31A



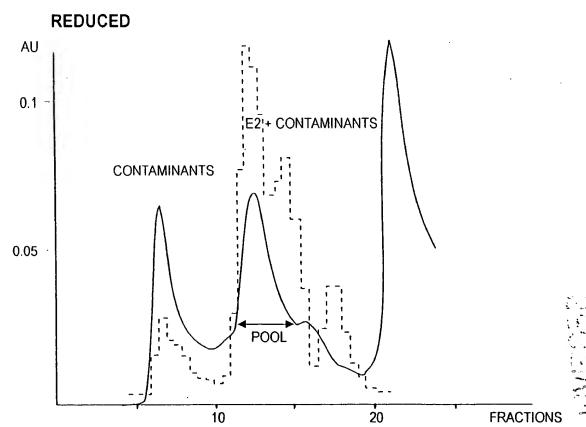


Fig. 31B



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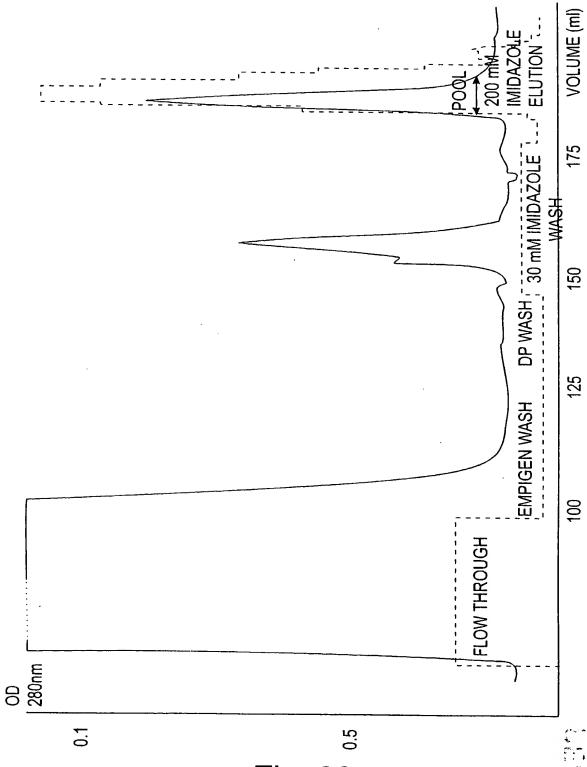
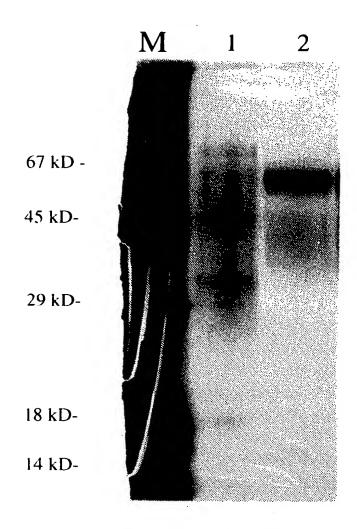


Fig. 32



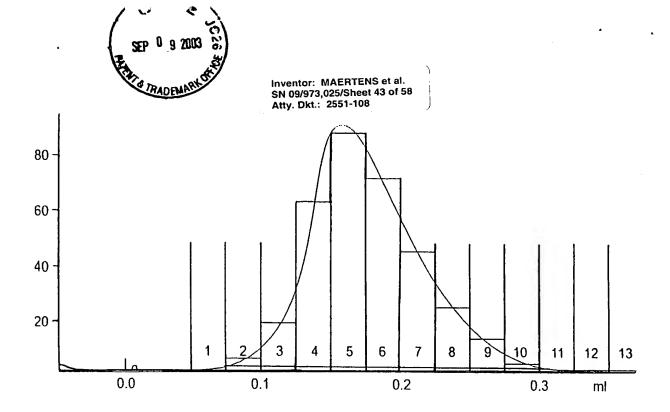
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### SILVER STAIN OF PURIFIED E2



- 1. 30 mM IMIDAZOLE WASH Ni-IMAC
- 2. 0.5 ug E2

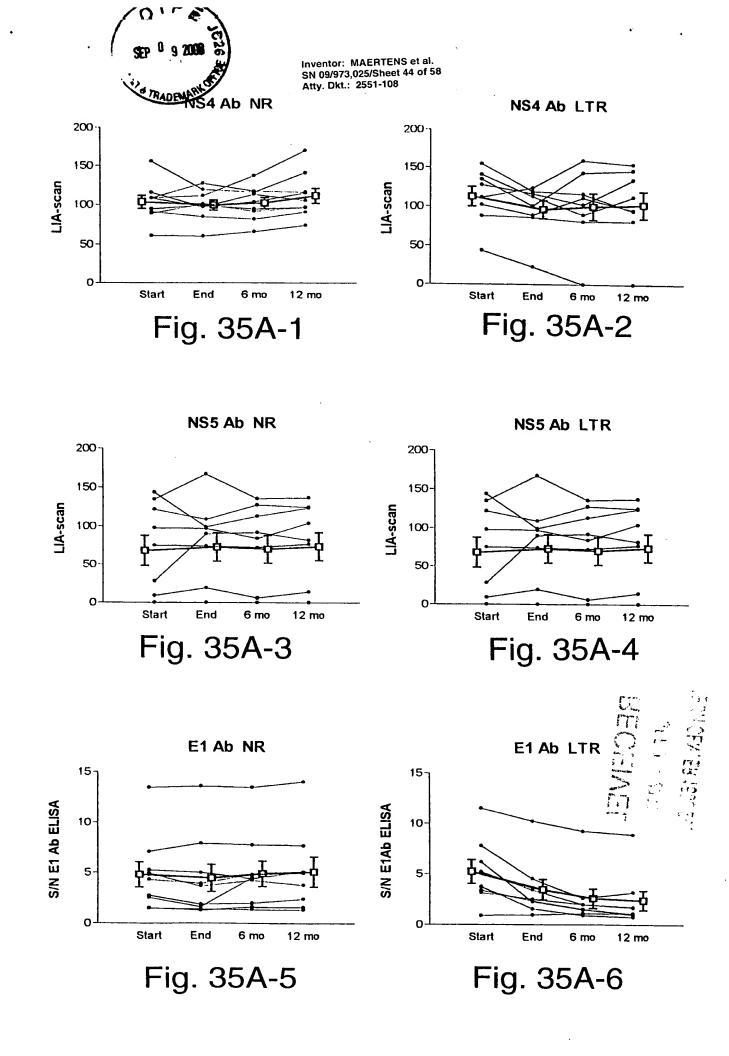
Fig.33



No.	Ret. (ml)	Peak start (ml)	Peak end (ml)	Dur (ml)	Area (ml*mAU)	Height (mAU)
1	-0.45	-0.46	-0.43	0.04	0.0976	4.579
2	1.55	0.75	3.26	2.51	796.4167	889.377
3	3.27	3.26	3.31	0.05	0.0067	0.224
4	3.33	3.32	3.33	0.02	0.0002	0.018

Total number of detected peaks = 4
Total Area above baseline = 0.796522 ml\*AU
Total area in evaluated peaks = 0.796521 ml\*AU
Ratio peak area / total area = 0.999999
Total peak duration = 2.613583 ml

Fig. 34





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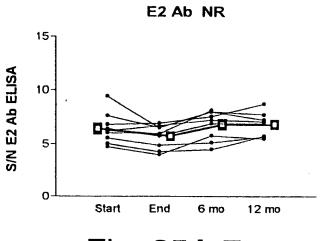


Fig. 35A-7

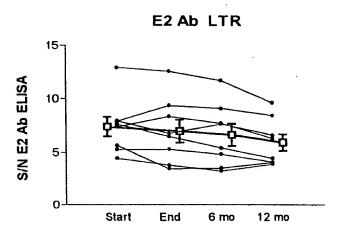


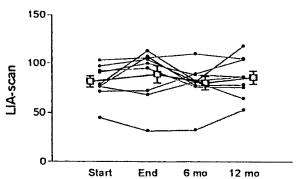
Fig. 35A-8



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Core 1 Ab NR



Core 1 Ab LTR

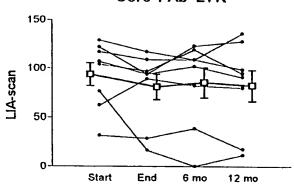
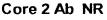
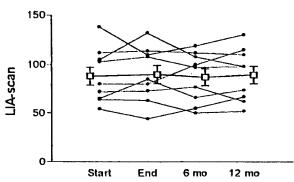


Fig. 35B-1

Fig. 35B-2





Core 2 Ab LTR

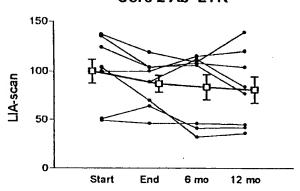


Fig. 35B-3



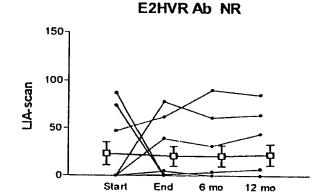


Fig. 35B-5

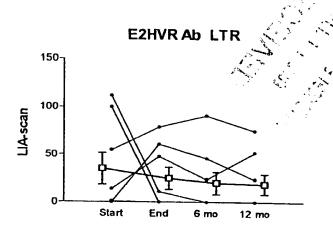


Fig. 35B-6



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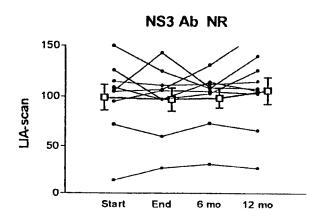


Fig. 35B-7

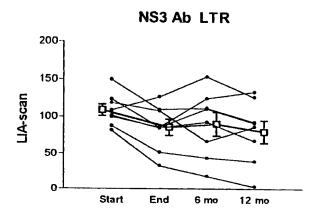


Fig. 35B-8



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## Fig. 36A

## E1 Ab

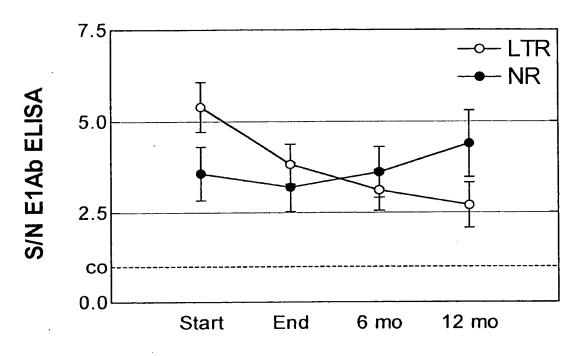
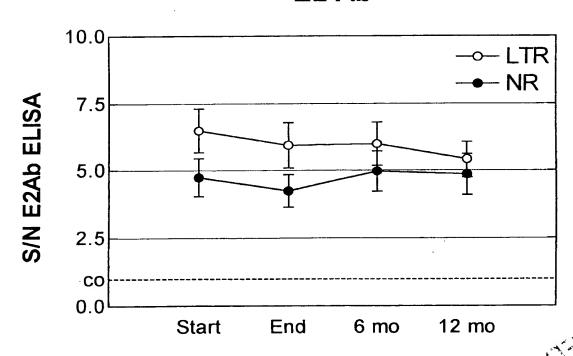
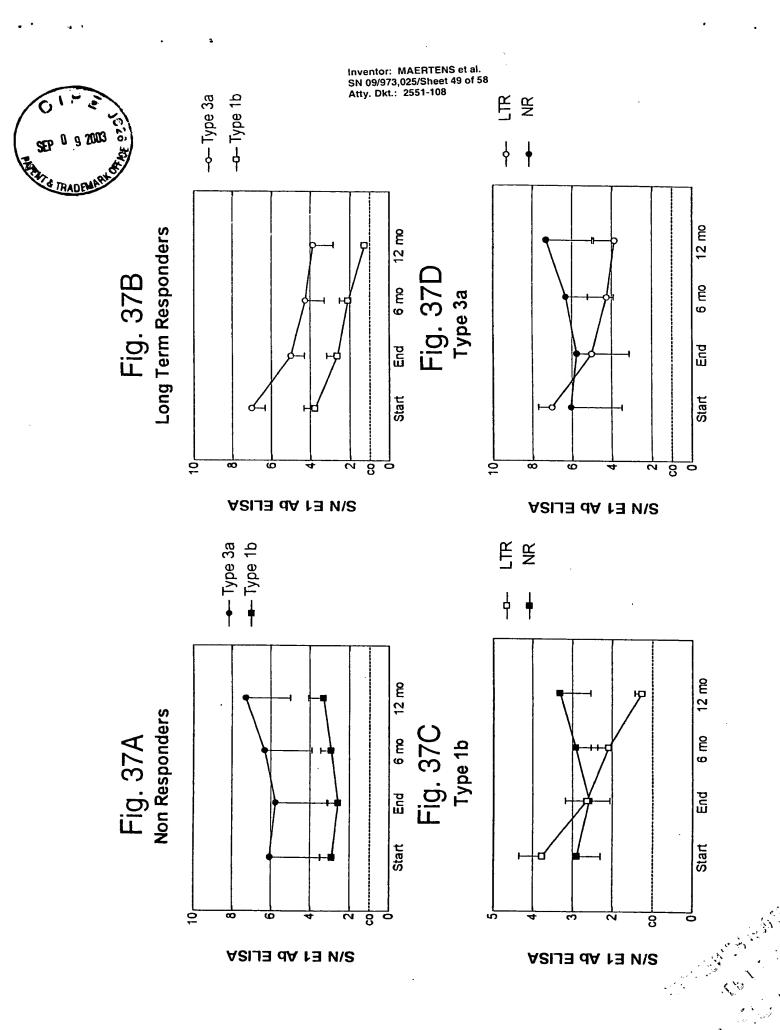


Fig. 36B **E2 Ab** 





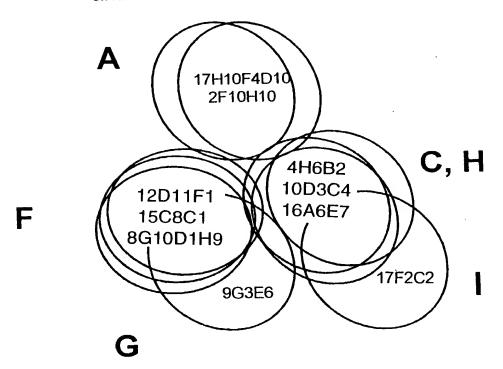


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Fig. 38

Relative Map Positions of anti-E2 monoclonal antibodies

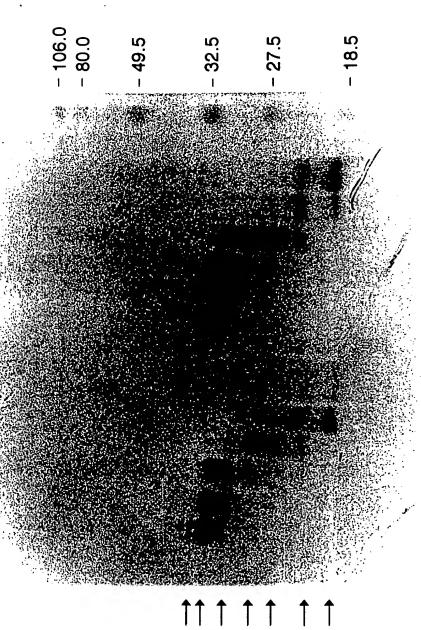


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Fig.39

# PARTIAL DEGLYCOSYLATION OF HCV E1 ENVELOPE PROTEIN

nw00+ Glycopeptidase F (PNGase F) nm04 ոաե um4.0 um<del>1</del>0.0 ոաօ Endoglycosidase H (Endo H) ոաց uma.0 ոա*ൻ*09 n*1*19 n*r*l9:0 n*r*l0





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# PARTIAL TREATMENT OF HCV E2\E2S ENVELOPE PROTEINS BY PNGase F

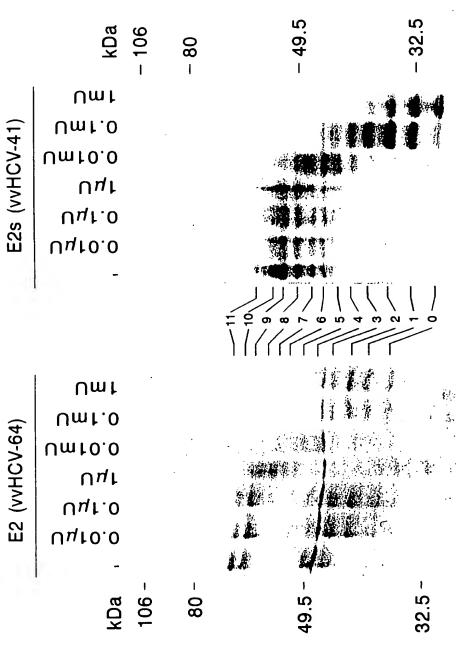
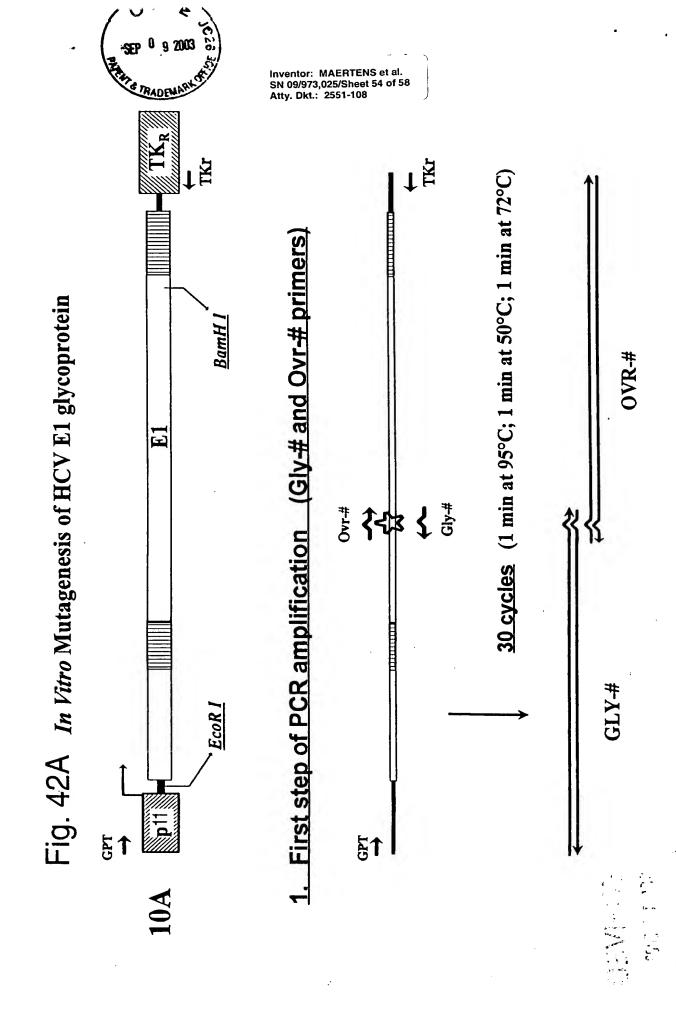


Fig. 40

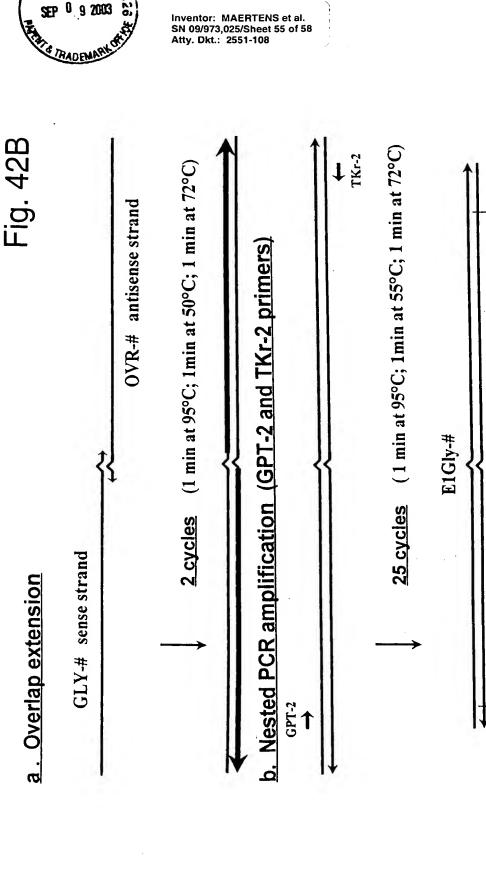
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Fig. 41 In Vitro Mutagenesis of HCV E1 glycoprotein

E1Gly-3 E1Gly-2 E1Gly-4 E1Gly-5 TKr 384 BamH. **@** 엃 6 **E**1 Stu I Sac I <del>@</del> Sac I <u></u> Bsp E I 0  $\Theta$ ///p11 p11 **p**11 p11 // J11 CORE **†**GPT I-W: E. coli gpt أشارا والأرام 1600 2800 F 82 85 83 84 98 10A81



2. Overlap extension and nested PCR

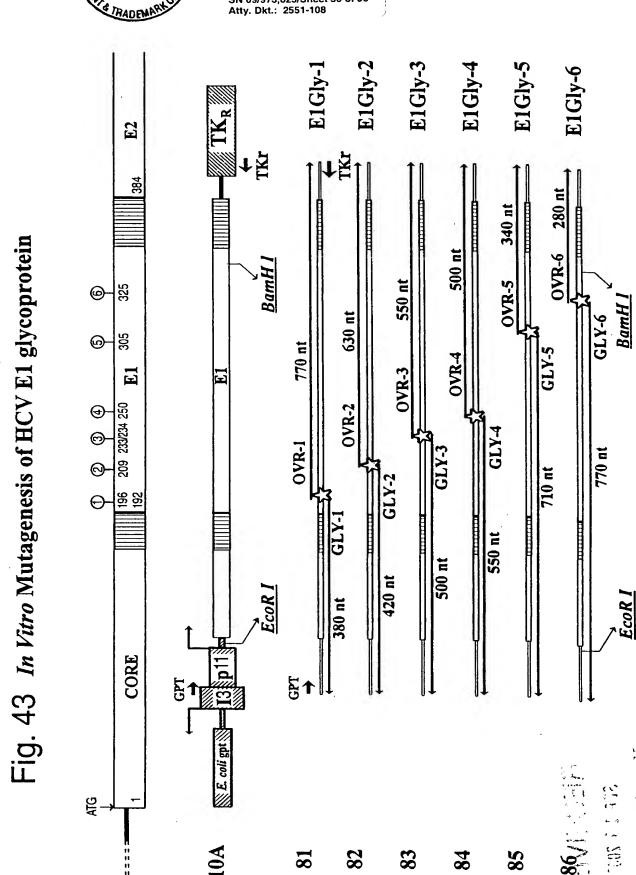


Bam HI

EcoR I

SEP 0 9 2003

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### RK 13 cells HeLa cells 3 80,0 80,0 80,0 49.5 49.5 49.5 32.5 32.5 32.5 27.5 27.5 27.5 18.5 18.5 18.5

Fig. 44A

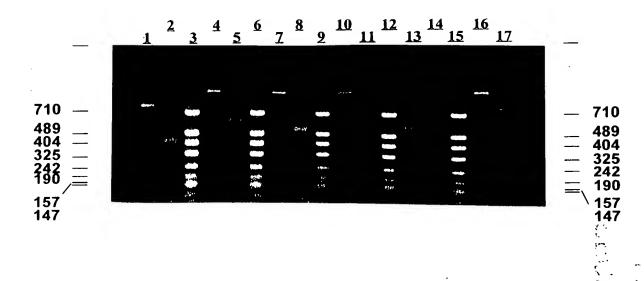


Fig.44B



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Fig. 45

KDall9 67 43

Fig.46